


Report and Recommendations of Animal Agriculture Stakeholders

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*Outlining priorities in the area of
animal pathogen genomics and
providing recommendations to the
USDA for leadership opportunities*

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Foreword

This is a report from the recently concluded USDA stakeholder electronic workshop for the prioritization of animal pathogens for genomic analysis and recommendations to the USDA for providing leadership in the area of animal pathogen genomics.

An effort jointly supported by the Agricultural Research Service (ARS) and the Cooperative State Research, Education and Extension Service (CSREES) was initiated during May of 2000 to help guide the USDA as it continues to develop its intramural and extramural microbial genomics programs. It was conducted using an electronic (email) conference format so the process was broad in scope, cost-efficient and minimally intrusive to all participants. The workshop's website can be found at: <http://genome.cvm.umn.edu/>.

Administrative contacts for the workshop were Peter Johnson (USDA-CSREES; pjohnson@reeusda.gov) and Steve Kappes (USDA-ARS; smk@ars.usda.gov). Carole Bolin (Michigan State University), Brad Fenwick (Kansas State University), and Vivek Kapur (University of Minnesota) served as co-chairs for this effort.

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Participating Panelists

A group of 26 internationally recognized investigators with diverse species specialization (e.g., dairy & beef cattle, swine, poultry, small ruminants, horses, and fish) was empanelled. The panelists who participated in this effort were:

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Executive Summary

Microbial diseases consistently rank among the most significant factors affecting human and animal health and the total annual costs associated with diseases due to microbial agents are in the tens of billions of dollars. In general, improvements in infectious disease prevention occur through the development of vaccines, antimicrobial agents, and diagnostic reagents. Thus far, the specific targets for these prophylactic, therapeutic or diagnostic agents have been discovered primarily through a combination of serendipitous and experimental identification of antigens, virulence factors, and other drug targets. These approaches are slow and laborious, and to a certain extent, depend on chance. Thus, there is a critical need to obtain a better understanding of the molecular basis by which microbial pathogens cause disease in and interact with their hosts.

Whole-genome sequencing is a powerful method for rapidly identifying all of the genes of a microbe and serves as the basis for future functional analyses of the newly discovered genes. The foundation of this program rests on the comprehensive identification of all of the genes in the pathogen in order to identify proteins that are responsible for virulence, pathogenesis, host specificity, and the induction of protective immune responses. Recent advances in microbial genomics provide strong evidence that *large-scale analysis of the microbial pathogen genome will identify novel antigens, biochemical pathways, and virulence mechanisms that are critical for pathogen survival, disease pathogenesis, and immunity. It is widely recognized that this in turn will provide the basis for designing new and effective vaccines, antimicrobial agents, and diagnostic reagents to help prevent and control infectious diseases.*

In order to provide the USDA with recommendations for how to proceed in harnessing the tremendous opportunities provided by this new and exciting field of microbial genomics, *a workshop of well-recognized scientists from throughout the world was brought together in an electronic conference and have put together:*

- *A priority list of 15 animal health & food safety pathogens that would benefit from microbial genomics, including a brief rationale for the classification (e.g., economic relevance and scientific rationale).* It was recognized that the sequencing of one or more of these high-priority organisms may already be funded for the sequence to be available in the public domain at the time of release of this report. To obviate the datedness of these lists, a framework for a semi-annual international review of the “high-priority” organisms was suggested. It was also acknowledged that the lack of inclusion on this list should not imply that a microorganism is undeserving of consideration for funding.
- *Suggestions/ recommendations offered to the USDA on its role (both intramurally and extramurally) for microbial genomics, including guidance for future proposal solicitations and ongoing prioritization strategies.* The USDA is urged to more deeply engage its activities in the area of microbial genomics, functional gene analysis, and bioinformatics in order to harness the tremendous opportunities afforded by technological and scientific advances in these areas of inquiry.

Specific recommendations include:

- (i) Development of a strategic plan for intramural and extramural research in the area of microbial genomics;
- (ii) Allocation of sufficient resources for peer-reviewed research on sequencing and functional genomic analysis of high-priority organisms over the next five years (a minimum of \$90 million: \$15 million in year one; \$16.5 million in year two; \$18.5 million in year three; and \$20 million each in years four and five);
- (iii) Development of a uniform data release policy that encourages early public disclosure of sequence and gene expression analysis data;
- (iv) Development of infrastructure and resource facilities for the archival and dissemination of shared resources including culture strains, genomic and expression libraries, plasmids, oligonucleotide primers and reagents for microarray analysis;
- (v) Development and maintenance of community access computer databases for the dissemination of sequencing and related information;
- (vi) Continued support of international workshops in the area of microbial genomics to foster exchange of information and encourage the development of a strong community in the area of microbial genomics of animal pathogens;
- (vii) Sufficient training resources (e.g., postdoctoral fellowships; sabbaticals; short courses) to assure adequate numbers of animal and veterinary biologists with expertise in functional and structural genomics techniques, as well as computational biology; and,
- (viii) Allocation of funds to support outreach efforts to the general public, including consumers, students, and agricultural professionals, to better educate them about the power and promise of microbial genomics.

Finally, an important outcome of this electronic conference has been to provide a mechanism for enhanced national and international coordination for animal microbial genomics among the research community, professional organizations, commodity organizations, and other stakeholders.

Objectives of the Workshop

The panelists were requested to address two major areas of relevance to the field of microbial genomics relative to animal health and well-being:

1- Prioritization of Animal Pathogens for Genomic Analyses

Participants were asked to prioritize animal pathogens (bacteria, mollicutes, parasites, fungi) for microbial genomics research into three groups (high, medium, and low priority). Strategies that could be used to prioritize and coordinate future national and international efforts for veterinary microbial genomics were also requested to be developed.

2- Recommendations to the USDA for providing Leadership in Microbial Genomics

The USDA-CSREES' recently released "Microbe Genomics" call for proposals (www.reeusda.gov/ifafs) was to be discussed and suggestions for future solicitations proposed. Participants were also encouraged to recommend ways the USDA could provide strong leadership in pathogen genome sequencing, functional genomics, structural genomics, and proteomics.

The workshop has now ended and the results of these discussions and panel recommendations are provided herein.

Introduction

Microbes are awesome. This is in part because of their tremendous genetic, metabolic, and physiological diversity. They have a rich history: they were very likely the first forms of free-living life on Earth, and predate animals and plants by more than 3 billion years. Microbes are widely regarded as the foundation of the biosphere and comprise ~ 60% of the Earth's total biomass. Microbes also contribute substantially to human and animal suffering, accounting for more than 13 million deaths each year in humans, and a very considerable fraction of mortality and morbidity in domesticated and wild animals.

Recent advances in microbial genomics, combined with the long evolutionary and scientific history of microbes, particularly of those that are associated with disease in animals and people, provide a wonderful foundation for asking fundamental questions related to microbial pathogenesis. It is with this background that it is becoming increasingly well recognized that the USDA has a unique opportunity to capitalize on the power of microbial genomics to make considerable advances in the prevention of animal diseases and sustaining animal well-being.

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A recent interagency report on the federal investment in microbial genomics prepared by the White House Subcommittee on Biotechnology has summarized the activities and interests of several federal agencies in microbial genomics and have identified opportunities for and limitations to research in microbial genomics. A complete copy of the report is available at the URL:
www.whitehouse.gov/WH/EOP/OSTP/html/microbial/nsf00203_1.html.

This current report focuses on providing recommendations to the USDA to harness the tremendous opportunities afforded by whole genome sequencing and subsequent functional analyses of microbial genomes. This document outlines a priority list of animal pathogenic microbes that the scientific and stakeholder community have identified for targeted genome sequencing and provides a rationale for the same. This report also provides a suggested framework for the USDA to assume a leadership role in the area of sequencing of microbial pathogens that are relevant to animal health and food safety.

Ongoing genome sequencing projects on animal and food safety pathogens

A review of the public information databases shows that about 35 of the more than 130 microbial genomics projects that are completed or underway include animal health or food-safety related organisms (listed below). An updated list of ongoing microbial genome sequencing projects is available at the URL: www.tigr.org.

Organism	Funding Source	Sequencing Center
<i>Anaplasma marginale</i>	USDA-ARS	ARS/ Washington State Univ./ Amplicon Express, Inc.
<i>Ascaris suum</i> - ESTs	Beowulf	Univ Edinburgh/ Sanger Centre
<i>Bacillus anthracis</i>	ONR/DOE/NIH	TIGR
<i>Bordetella bronchiseptica</i>	Beowulf	Sanger Centre
<i>Brucella abortus</i>	USDA-ARS	ARS
<i>Brucella melitensis</i>	Congressional Appropriation	Univ. Scranton
<i>Brucella suis</i>	DOD-DARPA / NIAID	TIGR
<i>Burkholderia mallei</i>	DOD-DARPA	TIGR
<i>Burkholderia pseudomallei</i>	Beowulf	Sanger Centre
<i>Campylobacter jejuni</i>	EU	Institut Pasteur
<i>Clostridium botulinum</i>	Beowulf	Sanger Centre
<i>Clostridium difficile</i>	Beowulf	Sanger Centre
<i>Clostridium perfringens</i>	University of Tsukuba	Japan*
<i>Cowdria ruminantium</i>	NOW WOTRO	Sanger Centre
<i>Cryptosporidium parvum</i>	NIH	University of Minnesota
<i>Escherichia coli</i> O157:H7	NIH	University of Wisconsin
<i>Haemonchus contortus</i> - ESTs	Beowulf	Univ Edinburgh/ Sanger Centre
<i>Lawsonia intracellularis</i>	USDA-CSREES-IFAFS	University of Minnesota
<i>Listeria monocytogenes</i>	EU	Institut Pasteur*
	USDA-ARS	TIGR
<i>Mannheimia haemolytica</i>	USDA/CSREES/NRI	Baylor Coll. Med.
	Privately Funded	Moredun Institute*
<i>Mycobacterium bovis</i>	Beowulf	Sanger Centre
<i>Mycobacterium paratuberculosis</i>	USDA/CSREES/NRI	University of Minnesota and ARS
<i>Mycoplasma gallisepticum</i>	Univ of Connecticut	Institute for Systems Biology
<i>Mycoplasma hyopneumoniae</i>	Iowa State	Iowa State University
<i>Neospora caninum</i> EST and GST	USDA-CSREES-NRI	Washington Univ.
<i>Pasteurella multocida</i>	USDA-CSREES-NRI ; Univ. Minn. ; MN Turkey Growers	University of Minnesota
<i>Pseudomonas aeruginosa</i>	CF Foundation/PathoGenesis	University of Washington
<i>Salmonella enteritidis</i>	Univ. of Illinois	University of Illinois
<i>Salmonella</i> spp. dublin, cholera suis, pullorum (low coverage)	USDA/CSREES/NRI	University of Illinois
<i>Salmonella typhi</i>	Beowulf	Sanger Centre
<i>Salmonella typhimurium</i>	NIH	Washington Univ. Consortium
<i>Streptococcus equi</i> ss equi	The Home of Rest for Horses	Sanger Centre
<i>Streptococcus agalactiae</i>	MENRT	Institut Pasteur
<i>Theileria parva</i>	Rockefeller/ ILRI/ USDA-ARS/TIGR	TIGR
<i>Toxoplasma gondii</i>	1 chromosome; EST	Sanger Centre ; Washington Univ.
<i>Trichinella spiralis</i>		Univ Edinburgh/ Sanger Centre

*Data not publically available

Priority List of Organisms Identified by the Panel based on Scientist and Stakeholder Input

The following is a list of organisms identified as candidates of high priority for whole genome sequencing by the panelists and external stakeholder groups. Also provided is a brief rationale for the placement of the organism in the high priority category. This list of 15 organisms was identified from a total of more than 100 pathogens that merit immediate investment in terms of whole genome sequencing as the anticipated return on invested time, effort, and money is deemed to be the greatest. The microorganisms primarily consist of bacterial genomes, and to a much lesser degree, protozoa. This is based largely on genome size and the costs associated with current techniques. Fungi, helminths, and arthropods are also important problems in animal health, but due to large genome size are given a current low priority. Viruses are of high relevance to animal health, but they were not considered by the panel because many have already been sequenced or could be relatively easily sequenced due to their small size. Nevertheless, the panel urges that adequate support for sequencing and functional genomics be available for all causes of animal disease, including viruses and other non-bacterial pathogens.

The following is the list of organisms identified as High Priority for Sequencing (listed in alphabetical order):

- *Actinobacillus pleuropneumoniae*- this is an important pathogen of swine; difficult genetic systems ; improved vaccines needed
- *Edwardsiella ictaluri*- causes an important disease of catfish
- *Eimeria* spp. (low coverage)-most important coccidian parasite; important pathogen in multiple species
- *Escherichia coli* (poultry septicemia strain: 078 or 02)-important disease in chickens and turkeys; clones are distinct from other *E. coli* isolates
- *Haemophilus paragallinarum*- causes an important disease of chickens
- *Haemophilus somnus*- causes an important disease of cattle; important in respiratory and neurological disease ; good comparative genomics model
- *Leptospira borgpetersenii* serovar *hardjo*-most important leptospiral pathogen in cattle globally; not genetically manipulable; important zoonoses
- *Mycoplasma bovis* – important cause of bovine mastitis ; no effective treatments or vaccines ; good comparative genomics model
- *Pasteurella multocida* (swine non-toxigenic strain)- important cause of disease in swine, no effective vaccines; good comparative genomics model

- *Renibacterium salmoninarum* – causal agent of bacterial kidney disease in Atlantic and Pacific salmon; major economic impact; no effective vaccines
- *Rhodococcus equi* – causes an important disease of horses; potential zoonosis; good comparative genomics model for mycobacteria and other intracellular bacteria; vaccines needed
- *Staphylococcus aureus* (bovine clones) – important mastitis pathogen
- *Streptococcus suis* - important disease of swine, multiple serotypes, no reliable vaccines
- *Streptococcus equi* ss *zooepidemicus* - important cause of equine disease
- *Toxoplasma gondii* (EST project in progress and one chromosome being sequenced)- model for apicomplexans such as *Eimeria*, *Sarcocystis*, *Neospora*, etc.; important zoonosis

Other Pathogenic Organisms Considered by the Panel based on Scientist and Stakeholder Input

The following is a list of organisms that were also considered when developing the priority list for whole genome sequencing by the panelists and external stakeholders. This list is categorized on the basis of animal host species with which the agent is most commonly associated.

Microbial Pathogens of Swine

Ascaris suum
Bordetella bronchiseptica (swine strain)
Brachyspira hyodysenteriae
Brachyspira pilosicoli
Clostridium perfringens type C
Eperythrozoon suis
Erysipelothrix rhusiopathiae
Escherichia coli-porcine neonatal
diarrheal strain
Escherichia coli-porcine post-weaning
K88
Escherichia coli-porcine bowel edema
strain
Eubacterium suis
Haemophilus parasuis
Leptospira interrogans serovar pomona
Pasteurella multocida swine clones
Staphylococcus hyicus
Trichinella spiralis

Microbial Pathogens of Cattle

Arcanobacterium pyogenes
Babesia spp.
Bacteroides sp.
Campylobacter fetus ss *venerealis*
Clostridium chauvoei
Cowdria ruminantium
Dermatophilus congolensis
Enterococcus sp (mastitis)
Escherichia coli (septicemic calf O78)
Fusobacterium necrophorum
Moraxella bovis
Mycoplasma mycoides spp. *mycoides*
Ostertagia ostertagi
Pasteurella multocida (bovine)
Streptococcus agalactiae
Streptococcus dysgalactiae
Streptococcus parauberis
Streptococcus uberis
Theileria parva

Microbial Pathogens of Poultry

Actinobacillus salpingitidis
Bordetella avium
Chlamydomphila psittaci
Clostridium colinum
Clostridium perfringens type A (necrotic enteritis)
Mycoplasma iowae
Mycoplasma meleagridis
Mycoplasma synoviae
Ornithobacterium rhinotracheale
Reimerella anatipestifer

Microbial Pathogens of Sheep and Goats

Brucella ovis
Chlamydomphila abortus
Corynebacterium pseudotuberculosis
Coxiella burnetii
Dichelobacter nodosus
Haemonchus contortus
Mycoplasma mycoides spp. *mycoides*
Pasteurella multocida small ruminant clones

Microbial Pathogens of Horses

Actinobacillus equuli
Ehrlichia equi
Ehrlichia risticii
Klebsiella pneumoniae
Sarcocystis neurona
Strongylus vulgaris
Taylorella asini
Taylorella equigenitalis
Theileria equi

Microbial Pathogens of Fish

Aeromonas hydrophila
Aeromonas salmonicida
Edwardsiella tarda
Flexibacter columnaris
Ichthyophthirius multifiliis
Myxobolus cerebralis
Perkinsus marinus
Streptococcus iniae
Vibrio anguillarum
Vibrio salmonicida
Yersinia ruckeri

Microbial Pathogens that Infect Other Miscellaneous Animal Species

Brucella canis
Clostridium tetani
Enterococcus faecium (probiotic strains)
Yersinia pseudotuberculosis

USDA's Leadership Role

It is well recognized that the future of animal agriculture in the United States, as well as the public perception of the wholesomeness of the food we produce, is intimately tied to advances in our understanding of the mechanisms by which pathogenic microorganisms persist in the environment and, under certain conditions, cause disease in animals and humans. ***The principles and considerations related to this fact necessitate a much broader and deeper engagement of the USDA in the area of microbial genomics, functional gene analysis, and bioinformatics in order to harness the tremendous opportunities afforded by technological and scientific advances in these areas of inquiry.***

It is instructive to note that of the more than 130 microbial genomics projects that have been completed or are underway, only 10 of those that are related to animal or food-borne disease are funded by the USDA. As noted earlier in this report, these represent only a small fraction of the nearly 100 other pathogenic microbes that are of importance to animal agriculture and threaten the safety and security of our food supply. Since it is now well accepted that the application of genomic analyses, including whole genome sequencing and functional genomics, will greatly enhance the quest to develop methods for prevention and control of these agents, we suggest that the USDA must publicly and explicitly engage and collaborate with other federal agencies and international organizations in ways that recognize the importance of this area of research in order to develop a comprehensive strategy to capitalize on these opportunities in microbial genomics.

It is well recognized that the research and analytic capacity of the USDA and affiliated university-based scientists is extraordinary. It is therefore with great conviction that we believe that the USDA is well positioned to play a central role in working with other groups to support the development of critical programs in advanced genomic analysis, data management, information transfer and translational research, education, and other related areas of genetic and genomics-related research.

In order to accomplish this, we believe that the USDA needs to develop a focussed program in the area of animal microbial genomics. Since there is a natural and desirable overlap in this area with other federal agencies such as the NIH, NSF, DOE, and others, a coordinated strategic approach comparable to what was developed to support the human genome project should be considered. The scientific rationales, as well as the economies that justify the approach used to sequence the human genome, apply equally to the challenge of understanding the genetics of microorganisms of agricultural importance. Although on a smaller scale, as with the human genomic project, such efforts by the USDA will necessarily require the infusion of new funding in order to be successful and to prevent undermining ongoing research programs. This approach has the greatest potential of leveraging the intellectual and physical resources of the USDA in collaboration with the public and private organizations that have vested interests in the production of a wholesome food supply of reasonable cost for the public of the United States and the world.

Panel Recommendations

Based on scientific discussions and stakeholder input, the panel has developed a series of recommendations for the USDA to take leadership in the area of microbial genomics of animal pathogens. These recommendations are:

- ***Development of a strategic plan for intramural and extramural research in the area of microbial genomics.*** Amongst the most important short-term goals includes the development of a comprehensive and coordinated strategic plan for intramural and extramural research in microbial genomics. We encourage the USDA to develop a strategy similar to the successful multi-agency approach adopted by the National Human Genome Research Institute of the National Institutes of Health for large-scale genome sequencing projects in order to develop this area as rapidly as possible and with the widest impact in terms of resource and infrastructure development.
- ***Immediate allocation of sufficient resources for peer-reviewed investigator-initiated research on sequencing and genomic analysis of high-priority organisms.*** A paucity of resources is currently allocated in this area by the USDA. Similar to what was recently accomplished by the USDA's Initiative for Future Agriculture and Food Systems (www.reeusda.gov/ifafs) and the NIH's National Institute of Allergy and Infectious Disease (www.niaid.nih.gov/dmid/genomes/priorities.htm), we encourage the USDA to develop an independent funding mechanism for the sequencing of animal pathogen microbes. This program should encourage and consider for funding research applications for large-scale genome sequencing and analysis of microbial pathogens that have been identified by the stakeholders in the high-priority list. Based on the estimated genome size of the 15 pathogens on the high-priority list, and cost per finished base for the bacterial pathogens, and per EST for the protozoan parasites, and our conservative estimates of the funds required over a five-year period for structural and functional genomics projects for the high-priority organisms that have been identified herein, *we encourage the USDA to allocate a minimum of \$90 million over the next five years (\$15 million in year one; \$16.5 million in year two ; \$18.5 million in year three ; and \$20 million each in years four and five) for the focused microbial genomics program.* These funds and the projected increase in requirements reflect the fact that during later years an increasing amount of effort on functional genomics and translation of the products of genomics research into better diagnostic tests, drugs and vaccines will require a larger investment than the acquisition of genomics sequence data which is more readily accomplished. It is recognized that the organisms on the high-priority list will frequently change, therefore, we propose that the USDA empanel an international working group with the charge of updating the list of organisms on a semi-annual basis. We also acknowledge that the lack of inclusion on this list should not imply that a microorganism is undeserving of consideration for funding.

- ***Development of a uniform data release policy that encourages early public disclosure of sequence and gene expression analysis data.*** The panel recognizes that early public access to gene sequencing and expression analysis data are key components to the successful development of microbial genomics programs in the scientific community. To this end, the panel recognizes that large-scale genome sequence information is a valuable research resource and that rapid and unrestricted sharing of microbial genome sequence data is required for advancing research on animal and food safety pathogens and accelerating the pace of experimental discovery. Hence, we encourage the USDA to develop and adopt a uniform policy on data release similar to what has recently been adopted by the NIH's NIAID (<http://grants.nih.gov/grants/guide/notice-files/not99-040.html>) that provides a framework for the early public release of sequence data whilst protecting the intellectual property rights of individual investigators as outlined in the Bayh-Dole Act.
- ***Development of infrastructure and resource facilities for the archival and dissemination of shared resources including culture strains, genomic and expression libraries, plasmids, oligonucleotide primers and reagents for microarray analysis.*** In order to accelerate the dissemination of knowledge and the pace of discovery in the field of animal pathogen genomics, the panel encourages the USDA to consider development of the required infrastructure and resource facilities for archival and dissemination of shared resources. It is anticipated that these shared resources will include culture strains and collections, genomic and expression libraries, plasmids, oligonucleotide primers and reagents for microarray based gene expression analyses, and other resources for proteomics and functional genomics research.
- ***Development and maintenance of community access computer databases for the dissemination of sequencing and related information.*** Consistent with the importance of rapid dissemination of information related to animal pathogen microbial genomics, we encourage the USDA to fund the development and maintenance of community access computer databases to enhance dissemination of animal pathogen sequencing and genomics related information along with providing easy access to bioinformatics tools needed for interpretation and mining of the genomic data.
- ***Continued support of workshops in the area of microbial genomics to foster exchange of information and encourage the development of a strong community in the area of microbial genomics of animal pathogens.*** The panel recognizes that the ultimate utility of the information derived from an animal pathogen microbial genomics initiative will be facilitated by the development of a strong community that utilizes that tremendous resources and opportunities afforded by this field. To this end, the panel encourages the USDA to continue to support user and stakeholder workshops in animal pathogen microbial genomics including those that specifically provide training in the areas of microbial genomics and bioinformatics.
- ***Allocation of sufficient training resources (e.g., postdoctoral fellowships; sabbaticals; short courses) to assure adequate numbers of animal and veterinary***

biologists with expertise in functional and structural genomics techniques, as well as computational biology. The panel believes that the greatest likelihood of developing a strong and productive scientific community that will harness the information resulting from a focussed genomic effort is through the training of future generations of scientists and hence recommends the allocation of sufficient training resources.

- *Allocation of funds to support outreach efforts to the general public, including consumers, students, and agricultural professionals, to better educate them about the power and promise of microbial genomics.* The Panel believes that an informed and supportive public is central to the continued success of this or any publicly-funded program. Hence, we recommend that the USDA should allocate sufficient resources to support outreach and other community education and development efforts.

Appendix 1: Stakeholder Organizations Invited to Participate

American Association of Avian Pathologists
American Academy of Microbiology
American Academy of Virologists
American Association of Avian Pathologists
American Association of Bovine Practitioners
American Association of Equine Practitioners
American Association of Swine Practitioners
American Association of Veterinary Laboratory Diagnosticians
American Association of Veterinary Medical Colleges
American Association of Veterinary Parasitologists
American Association of Veterinary Pathologists
American College of Veterinary Preventive Medicine
American Farm Bureau Federation
American Horse Council
American Meat Institute
American Sheep Industry Association
American Society of Parasitologists
American Veterinary Medical Association
Canadian National Research Council
Federation of Animal Science Societies
Microcide Pharmaceuticals
National Cattlemen's Beef Association
National Milk Producers Federation
National Pork Producers Council
Pharmacia and Upjohn
US Academic Committee on Policy
US Animal Health Association
US 1890 Deans
US 1890 Extension Administrators
US 1890 Research Directors
US Cooperative Extension Directors
US Experiment Station Directors
US Experiment Station Regional Groups
US Landgrant Administrative Heads
US Poultry and Egg Association
Wellcome Trust- Beowulf Genomics

Appendix 1: – Contd.

US Federal Agencies:

National Aeronautics Space Agency
National Institutes of Health
National Science Foundation
US Department of Agriculture- APHIS
US Department of Agriculture- ARS
US Department of Agriculture- CSREES
US Department of Agriculture- FSIS
US Department of Defense
US Department of Energy

Invitations Extended Through Listservers to the following Discussion Groups:

Angenmap (animal genetics)
Beef-L
Conference of Research Workers in Animal Diseases
Dairy-L
EDN-L (equine clinicians)
PorkNet
ProMed
Swine-L
Vetimm (veterinary immunologists)
Vetmed
Vetmicro (veterinary microbiologists)

Appendix 2: Workshop Timeline

PLANNING & PREPARATION (November 1999 - April 2000)

- **November 1999:** An ad hoc group of researchers met with ARS and CSREES national program staff at the Conference for Research Workers in Animal Diseases in Chicago, IL to discuss the need for a coordinated approach to microbial genomics for animal pathogens. A workshop to prioritize animal pathogens was urged and the USDA agreed to facilitate a process that would allow the animal health community to provide stakeholder input to the Department of Agriculture. Three scientists subsequently agreed to represent the scientific community as co-chairs for an electronic workshop that would be international in scope.
- **December 1999:** The USDA administrative contacts and 3 co-chairs outlined a tentative implementation process.
- **January 2000:** A follow-up group of interested animal health researchers met with ARS and CSREES national program staff at the 1st International Agricultural Microbes Genome Conference in San Diego, CA to further develop the process for an electronic workshop.
- **February -April 2000:** Invitations were extended to panel members. Panel membership was balanced by geography, institution, commodity, discipline, and professional rank. An effort was made to identify as many qualified women and minorities as possible. Exact guidelines for the panel process, as well as estimated timelines, were finalized. Listservers were established at the University of Minnesota.

PHASE 1 (May - June 2000):

- **Panel input:** For a 4 week period, the panel interactively addressed the two areas previously highlighted using an email listserver. Participants' comments sent to this listserver were not "filtered" or "edited"; emails were automatically distributed to all other members of the panel. Panelists were strongly encouraged to consult broadly with colleagues and commodity partners who were not members of this stakeholder group, and to share that input with the rest of the panel. Panelists were asked to check their email for listserver comments at least once per day during the conference. The three co-chairs also contributed to the discussion and provided broad oversight to

Appendix 2: – Contd.

assure an efficient process. The USDA programmatic contacts provided logistical support as needed, and served as listeners and observers.

- ***Non-panel input*** (through a second listserver): To capture input from those not serving on the panel, as the panel discussion was occurring, a second listserver accepted input from non-panel members involved in animal health (e.g., other researchers, professional organizations, commodity partners, etc.). An invitation to participate (using a second listserver) was broadly distributed to the animal health user community. (See appendix 1.)

PHASE 2: (July - August 2000):

The 3 co-chairs generated a draft report which was shared with the other panel members (via the listserver) for further refinements. Simultaneously, the draft report was sent (electronically or by mail) to previously identified stakeholders (e.g., Animal Agriculture Coalition; AVMA; AAVMC, etc.) requesting written feedback within 4 weeks.

PHASE 3: (September – December 2000):

An executive "USDA Microbial Genomics Workshop 2000: Report and Recommendations of Stakeholders" was drafted by the 3 co-chairs and shared with the other panel members (via the listserver) for their input before finalizing this workshop. Information included in the list of "Ongoing genome sequencing projects on animal and food safety pathogens" (page 9) was updated through December 31, 2000 .

PHASE 4: (January 2001):

To assure equal access to the information by all interested parties, the report will be publicly available on the USDA-CSREES /ARS websites.

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